

Reference sequence:	AGCTCATTGA
Possible sub-sequences:	AGTCATTG
	GTCATTGA
	AGTCATT
	GTCATTG
	CTCATTGA

FIGURE 1

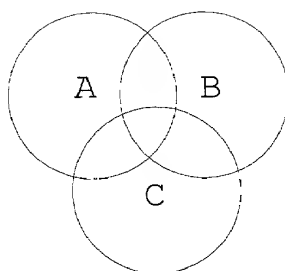


FIGURE 2A

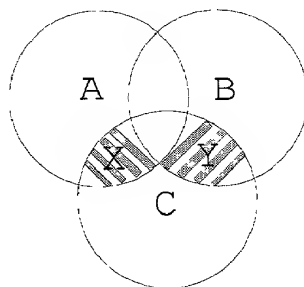


FIGURE 2B



FIGURE 3

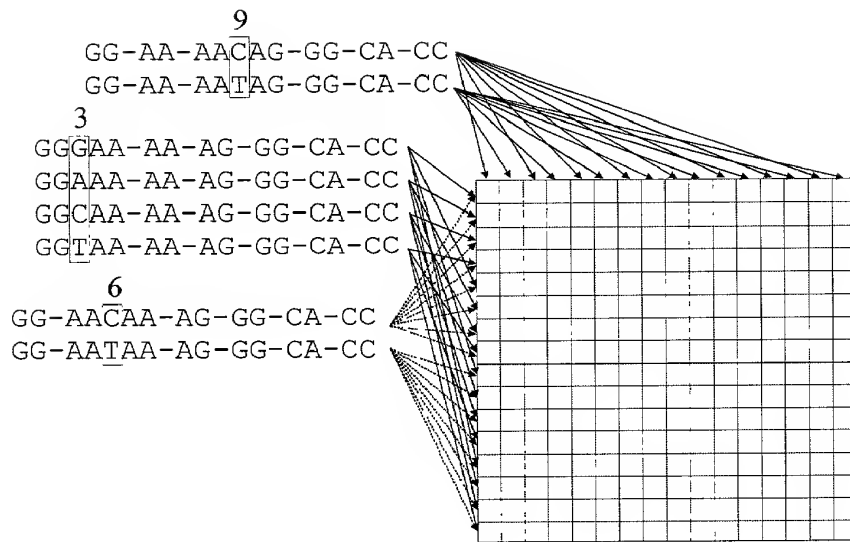
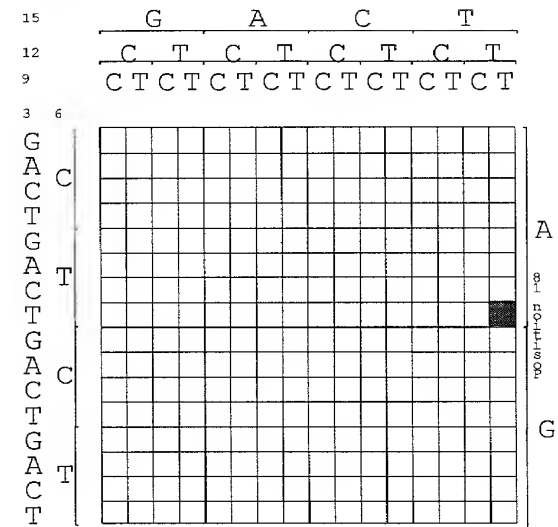
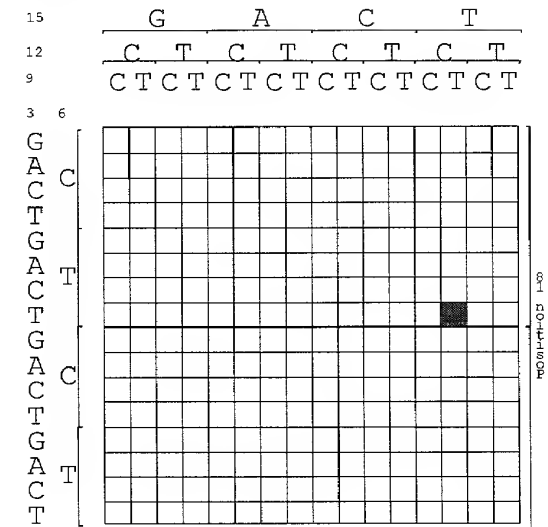


FIGURE 4

Positions



Positions



Positions

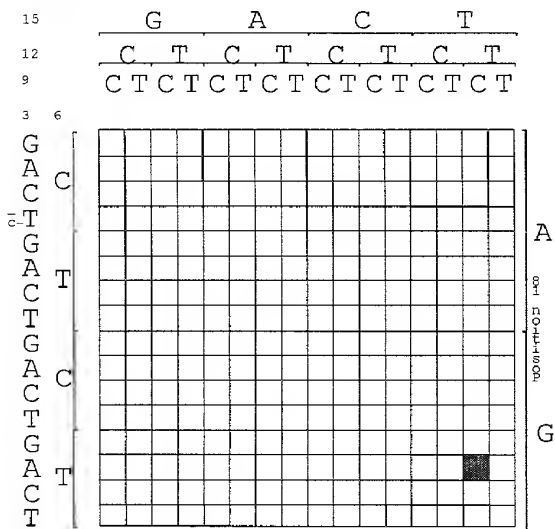


FIGURE 6A

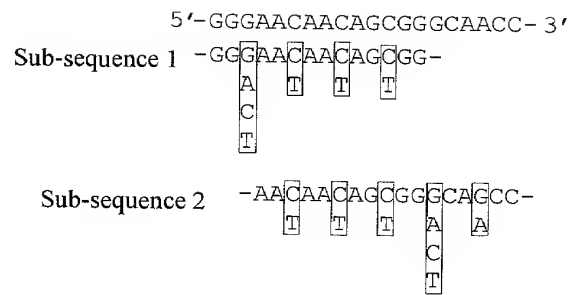


FIGURE 6B

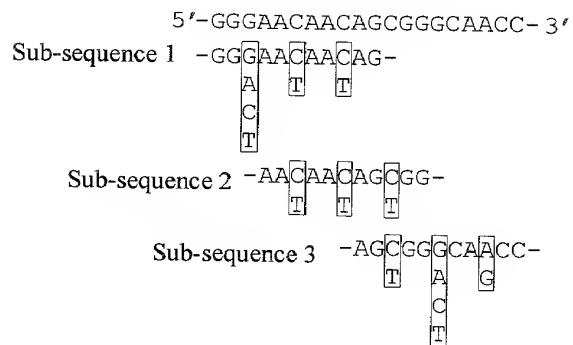


FIGURE 6C



FIGURE 6D



B motif

Positions

Position 3	9	C				T				9	C				T				9	G								A							
	6	C		T		C		T		6	C		T		C		T		6	G		A		T		C		G		A		C		T	
	G	1	2	3	4					3	C	17	18	19	20					3	C	25	26	27	28	29	30	31	32						
	A	5	6	7	8					T	21	22	23	24					T	33	34	35	36	37	38	39	40								
	C	9	10	11	12																														
	T	13	14	15	16																														

WCIEN motif

11	G				A				C					9	C			T			
9	G	A	T	C	G	A	C	T	G	A	C	T		6	G	A	C	G	A	C	
5	C	41	42	43	44	45	46	47	48	49	50	51	52		G	65	66	67	68	69	70
	T	53	54	55	56	57	58	59	60	61	62	63	64		A	71	72	73	74	75	76
															C	77	78	79	80	81	82
															T	83	84	85	86	87	88

NVED motif

3	12	C												T																			
	9	G				A				C				T				G				A				C				T			
	6	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T					
		89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112								
		113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136								

FIGURE 7

PVY-N PVY-NFR PVY-PA

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

PVY-Co

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

PVY-HUNG

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

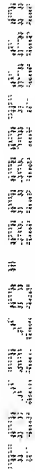
BYMV-S

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

PVY-NSW

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

FIGURE 8

[illegible]

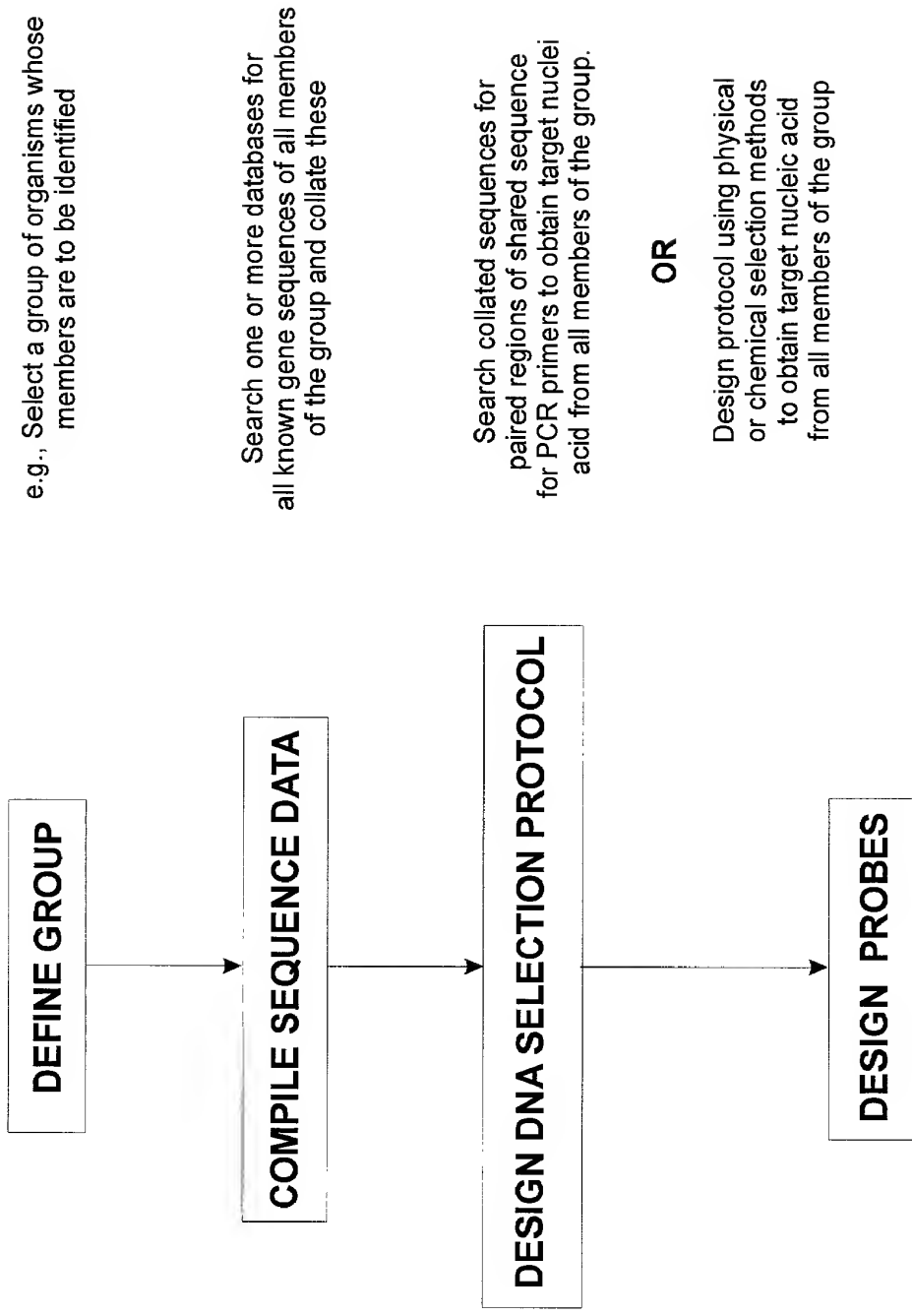


FIGURE 10

1. Fragment all sequences from all members of the group into all overlapping 'oligos' 8-12 or more nts long.

DESIGN PROBES

Fragment all sequences from all members of the group into all overlapping 'oligos' 8-12 or more nts long.

Prepare primary "taxon x oligo" matrix

Sort oligos into primary matrix recording presence of each kind of oligo (unique sequences) in each of the taxa (target sequences)

Deduce meta "taxon pair - oligo" matrix

Record, for each pair of taxa, the oligos that distinguish them

Identify 'minimum set cover' of oligo using 'greedy strategy'

1. Sum the 'hits' for each oligo in the meta-matrix;
2. Select and remove oligo that distinguishes most taxon pairs together with its 'hitting set';
3. Repeat 1. and 2. while progressively refining to obtain minimum best set.

Identify replicate sets of potential probes

Repeat selection process above to identify several minimum sets while progressively removing particular oligos as they are selected

EVALUATE DISCRIMINATORY POWER

Evaluate discriminatory power (both diagnostic and phylogenetic) of different combinations of potential probe sets 'in silico' and, finally, test the chosen sets 'in vitro'

FIGURE 10 contd.

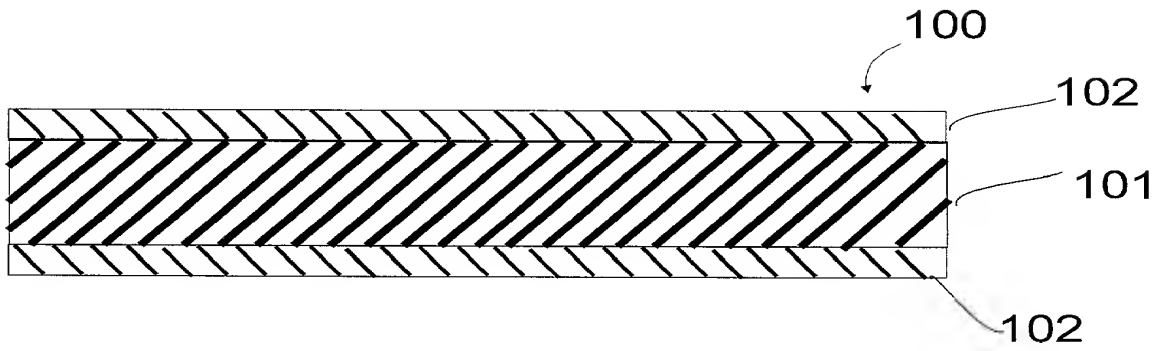


FIGURE 11

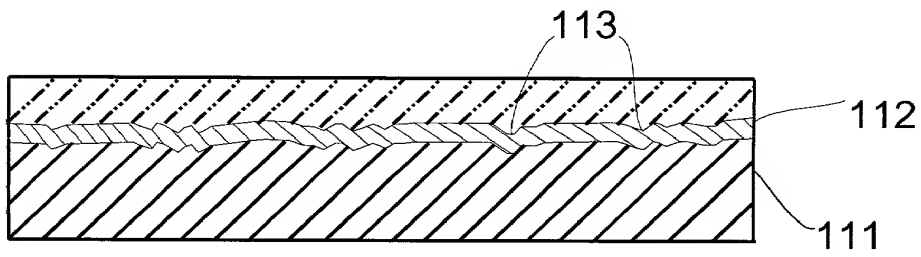


FIGURE 12